

SEQUENCE LISTING

<110> Conklin, Darrell C.
 Gao, Zeren
 Lofton-Day, Catherine E.
 Whitmore, Theodore E.

<120> SECRETED ALPHA-HELICAL PROTEIN ZLMDA24

<130> 00-94

<150> US 60/242,023

<151> 2000-10-20

<160> 25

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1041

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (205)...(966)

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| ctgagaacac cagaggactg gcagttggga gcctgatgga ggacaagtag ggcctcgagg | 60 |
| acaggtgcgt gacagaagca caggaaaaaa aagaaaaatg aagaaataaa aacacgagtt | 120 |
| catcagtaaa gaggtaccct ggcagcataa atattatgat aagctaaaag ctggaatcat | 180 |
| ctggaaaaat aaataagact cctc atg tcc ttt tcg gtc cat aac cag aag | 231 |
| Met Ser Phe Ser Val His Asn Gln Lys | |
| 1 5 | |

| | |
|---|-----|
| ggc agc aaa agg cct ttg cca ctg gaa cct ctt ctt ttt ctc caa gtc | 279 |
| Gly Ser Lys Arg Pro Leu Pro Leu Glu Pro Leu Leu Phe Leu Gln Val | |
| 10 15 20 25 | |

| | |
|---|-----|
| cca cgt agc aat tac ctg cac ttt caa gaa gag aaa caa cga cta cac | 327 |
|---|-----|

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Pro | Arg | Ser | Asn | Tyr | Leu | His | Phe | Gln | Glu | Glu | Lys | Gln | Arg | Leu | His | | |
| | | | | 30 | | | | | 35 | | | | | 40 | | | |
| cta | aag | aaa | ttc | ctt | ctt | gat | agg | atg | ttt | cta | gtg | gcc | aag | ata | caa | | 375 |
| Leu | Lys | Lys | Phe | Leu | Leu | Asp | Arg | Met | Phe | Leu | Val | Ala | Lys | Ile | Gln | | |
| | | | 45 | | | | | 50 | | | | | 55 | | | | |
| gca | aat | gta | gaa | aga | aaa | gat | gtt | gct | gac | tac | tat | gaa | caa | atg | ttt | | 423 |
| Ala | Asn | Val | Glu | Arg | Lys | Asp | Val | Ala | Asp | Tyr | Tyr | Glu | Gln | Met | Phe | | |
| | | 60 | | | | | 65 | | | | | 70 | | | | | |
| cag | tca | gtt | ttg | aaa | cat | cac | cta | gga | gaa | gca | gtg | aca | gga | ttg | ctg | | 471 |
| Gln | Ser | Val | Leu | Lys | His | His | Leu | Gly | Glu | Ala | Val | Thr | Gly | Leu | Leu | | |
| | 75 | | | | | 80 | | | | | 85 | | | | | | |
| ctc | atc | tat | ccc | act | tcc | att | ctg | cat | atc | ctc | gag | tcc | tcc | agc | gac | | 519 |
| Leu | Ile | Tyr | Pro | Thr | Ser | Ile | Leu | His | Ile | Leu | Glu | Ser | Ser | Ser | Asp | | |
| | 90 | | | | 95 | | | | 100 | | | | | | 105 | | |
| act | ctc | tac | aaa | gtt | ctt | tta | gat | tat | att | ggc | cat | gtc | aaa | gat | gaa | | 567 |
| Thr | Leu | Tyr | Lys | Val | Leu | Leu | Asp | Tyr | Ile | Gly | His | Val | Lys | Asp | Glu | | |
| | | | 110 | | | | | | 115 | | | | | 120 | | | |
| aca | gta | ttt | ttt | att | caa | caa | atg | aaa | att | ata | gtc | att | tct | cat | aac | | 615 |
| Thr | Val | Phe | Phe | Ile | Gln | Gln | Met | Lys | Ile | Ile | Val | Ile | Ser | His | Asn | | |
| | | 125 | | | | | 130 | | | | | 135 | | | | | |
| att | cca | atg | agg | ctt | ttt | atg | caa | tgg | cat | gtt | tca | gtg | ata | aaa | gtt | | 663 |
| Ile | Pro | Met | Arg | Leu | Phe | Met | Gln | Trp | His | Val | Ser | Val | Ile | Lys | Val | | |
| | 140 | | | | | 145 | | | | | 150 | | | | | | |
| cca | gtt | atg | tat | ctc | gac | gat | gtg | aca | cag | tca | cag | tcc | cta | aag | gag | | 711 |
| Pro | Val | Met | Tyr | Leu | Asp | Asp | Val | Thr | Gln | Ser | Gln | Ser | Leu | Lys | Glu | | |
| | 155 | | | | 160 | | | | | | 165 | | | | | | |
| gtc | atc | aca | gat | ttt | ctc | aca | caa | act | cat | aaa | ctg | tca | ctc | tac | ctt | | 759 |
| Val | Ile | Thr | Asp | Phe | Leu | Thr | Gln | Thr | His | Lys | Leu | Ser | Leu | Tyr | Leu | | |
| | 170 | | | | 175 | | | | | 180 | | | | | 185 | | |
| tgc | cag | act | atg | aaa | gta | ggc | act | aaa | gga | cca | ggc | gat | aac | tta | cac | | 807 |
| Cys | Gln | Thr | Met | Lys | Val | Gly | Thr | Lys | Gly | Pro | Gly | Asp | Asn | Leu | His | | |
| | | | 190 | | | | | 195 | | | | | | 200 | | | |

caa gtt gca cct gac cta ctc ctc cca gaa caa atc ata aag tac ttg 855
 Gln Val Ala Pro Asp Leu Leu Leu Pro Glu Gln Ile Ile Lys Tyr Leu
 205 210 215

tgc aaa tcc gaa gaa ttc atg gac ccg gca aca ttt ata aac atg tat 903
 Cys Lys Ser Glu Glu Phe Met Asp Pro Ala Thr Phe Ile Asn Met Tyr
 220 225 230

aat aga ccc ata cac atc act ctg gat tct gag gtg gta tgg cct gct 951
 Asn Arg Pro Ile His Ile Thr Leu Asp Ser Glu Val Val Trp Pro Ala
 235 240 245

cct tca cgt ttc tag gattgagagg gataatgtgc ccatgtctct taaggagttt 1006
 Pro Ser Arg Phe *
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gtgctactta aataaaaaaaaa acattttttaa agtta 1041

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 Phe Gln Glu Glu Lys Gln Arg Leu His Leu Lys Lys Phe Leu Leu Asp
 35 40 45
 Arg Met Phe Leu Val Ala Lys Ile Gln Ala Asn Val Glu Arg Lys Asp
 50 55 60
 Val Ala Asp Tyr Tyr Glu Gln Met Phe Gln Ser Val Leu Lys His His
 65 70 75 80
 Leu Gly Glu Ala Val Thr Gly Leu Leu Leu Ile Tyr Pro Thr Ser Ile
 85 90 95
 Leu His Ile Leu Glu Ser Ser Ser Asp Thr Leu Tyr Lys Val Leu Leu
 100 105 110
 Asp Tyr Ile Gly His Val Lys Asp Glu Thr Val Phe Phe Ile Gln Gln
 115 120 125
 Met Lys Ile Ile Val Ile Ser His Asn Ile Pro Met Arg Leu Phe Met
 130 135 140

Gln Trp His Val Ser Val Ile Lys Val Pro Val Met Tyr Leu Asp Asp
 145 150 155 160
 Val Thr Gln Ser Gln Ser Leu Lys Glu Val Ile Thr Asp Phe Leu Thr
 165 170 175
 Gln Thr His Lys Leu Ser Leu Tyr Leu Cys Gln Thr Met Lys Val Gly
 180 185 190
 Thr Lys Gly Pro Gly Asp Asn Leu His Gln Val Ala Pro Asp Leu Leu
 195 200 205
 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ser Glu Glu Phe Met
 210 215 220
 Asp Pro Ala Thr Phe Ile Asn Met Tyr Asn Arg Pro Ile His Ile Thr
 225 230 235 240
 Leu Asp Ser Glu Val Val Trp Pro Ala Pro Ser Arg Phe
 245 250

<210> 3
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<220>
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 <222> (106)...(867)

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 taccattgag acttgtaatc atctaaaaaa gaaataagat tcatc atg tct ttc atg 117
 Met Ser Phe Met
 1

gtc cat aat cgg aag ggc agc aaa aag caa ttt caa gtg gat cct ctt 165
 Val His Asn Arg Lys Gly Ser Lys Lys Gln Phe Gln Val Asp Pro Leu
 5 10 15 20

ctt ctg ccc aag gtt cct cgt acc aat tac ctg cac ctt cag gaa gag 213
 Leu Leu Pro Lys Val Pro Arg Thr Asn Tyr Leu His Leu Gln Glu Glu
 25 30 35

aag cac aga cta cag cta aag aaa ttc ctc ctt cac agg atg ttt cta 261
 Lys His Arg Leu Gln Leu Lys Lys Phe Leu Leu His Arg Met Phe Leu
 40 45 50

gtg ggc tac ata caa ggc aac acg gag aaa aag gac atc tct gag tac 309

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| Val | Gly | Tyr | Ile | Gln | Gly | Asn | Thr | Glu | Lys | Lys | Asp | Ile | Ser | Glu | Tyr | | |
| | | 55 | | | | | 60 | | | | | 65 | | | | | |
| tat | gag | caa | ctg | ttt | cag | tca | att | ctg | aaa | cat | cat | tta | ggc | gaa | tca | | 357 |
| Tyr | Glu | Gln | Leu | Phe | Gln | Ser | Ile | Leu | Lys | His | His | Leu | Gly | Glu | Ser | | |
| | 70 | | | | | 75 | | | | | 80 | | | | | | |
| gtg | aca | ggc | ctc | atg | ctc | gta | tac | cca | agt | act | ttt | ctg | cac | att | ctt | | 405 |
| Val | Thr | Gly | Leu | Met | Leu | Val | Tyr | Pro | Ser | Thr | Phe | Leu | His | Ile | Leu | | |
| | 85 | | | | 90 | | | | | 95 | | | | | 100 | | |
| gag | agt | tcc | aat | ggc | aca | ctc | ttc | cgg | att | ctt | cta | gat | tat | gtt | gcc | | 453 |
| Glu | Ser | Ser | Asn | Gly | Thr | Leu | Phe | Arg | Ile | Leu | Leu | Asp | Tyr | Val | Ala | | |
| | | | 105 | | | | | 110 | | | | | | 115 | | | |
| cat | gaa | aag | agt | gaa | aca | gaa | ttt | atg | ctc | caa | aac | atg | aaa | atc | gtt | | 501 |
| His | Glu | Lys | Ser | Glu | Thr | Glu | Phe | Met | Leu | Gln | Asn | Met | Lys | Ile | Val | | |
| | | 120 | | | | | 125 | | | | | 130 | | | | | |
| gtt | gct | tct | cac | aac | atc | ccc | acg | agg | ctg | ttc | atg | cag | tgg | cat | atc | | 549 |
| Val | Ala | Ser | His | Asn | Ile | Pro | Thr | Arg | Leu | Phe | Met | Gln | Trp | His | Ile | | |
| | 135 | | | | | 140 | | | | | | 145 | | | | | |
| tct | gca | atc | aaa | gtc | ccc | gtt | ttg | tac | cta | gat | gac | gaa | tca | cag | tct | | 597 |
| Ser | Ala | Ile | Lys | Val | Pro | Val | Leu | Tyr | Leu | Asp | Asp | Glu | Ser | Gln | Ser | | |
| | 150 | | | | 155 | | | | | | 160 | | | | | | |
| ccg | tct | ata | gag | gaa | gtc | acc | aca | gaa | ttc | ctc | acc | atg | act | cac | aaa | | 645 |
| Pro | Ser | Ile | Glu | Glu | Val | Thr | Thr | Glu | Phe | Leu | Thr | Met | Thr | His | Lys | | |
| | 165 | | | | 170 | | | | | 175 | | | | | 180 | | |
| ctg | gca | ctc | caa | ctt | tac | aag | aca | gtg | aaa | ttg | ggc | gcg | aaa | ggc | cca | | 693 |
| Leu | Ala | Leu | Gln | Leu | Tyr | Lys | Thr | Val | Lys | Leu | Gly | Ala | Lys | Gly | Pro | | |
| | | | 185 | | | | | | 190 | | | | | 195 | | | |
| ggc | gac | aac | tta | cac | caa | ctt | gcc | cct | gaa | ctc | att | ctc | cca | gaa | caa | | 741 |
| Gly | Asp | Asn | Leu | His | Gln | Leu | Ala | Pro | Glu | Leu | Ile | Leu | Pro | Glu | Gln | | |
| | | 200 | | | | | 205 | | | | | | 210 | | | | |
| att | atc | aag | tat | tta | tgc | aaa | gct | gaa | gaa | ttc | atg | gac | cca | gcg | tct | | 789 |
| Ile | Ile | Lys | Tyr | Leu | Cys | Lys | Ala | Glu | Glu | Phe | Met | Asp | Pro | Ala | Ser | | |
| | | 215 | | | | | 220 | | | | | 225 | | | | | |

Ala Lys Gly Pro Gly Asp Asn Leu His Gln Leu Ala Pro Glu Leu Ile
 195 200 205
 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ala Glu Glu Phe Met
 210 215 220
 Asp Pro Ala Ser Phe Leu Ser Met Tyr Asn Arg Pro Ile His Val Thr
 225 230 235 240
 Leu Asp Ser Asp Ile Val Trp Pro Ala Pro Ser Arg Phe
 245 250

<210> 5
 <211> 759
 <212> DNA
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 <223> Degenerate polynucleotide sequence of human z1mda24
 shown in SEQ ID NO:2

<221> misc_feature
 <222> (1)...(759)
 <223> n = A,T,C or G

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| atgwsnttyw sngtncayaa ycaraarggn wsnaarmgnc cnytnccnyt ngarccnytn | 60 |
| ytnttyytnc argtnccnmg nwsnaaytay ytncayttyc argargaraa rcarmgnytn | 120 |
| cayytnaara arttyytnyt ngaymgntatg ttytngtng cnaarathca rgcnaaygtg | 180 |
| garmgnaarg aygtngcnga ytaytaygar caratgttyc arwsngtnyt naarcaycay | 240 |
| ytnggngarg cngtnacngg nytnytnyt athtayccna cnwsnathyt ncayathytn | 300 |
| garwsnwnw sngayacnyt ntayaargtn ytnyngayt ayathggncay ygtnaargay | 360 |
| garacngtnt tyttyathca rcaratgaar athathgtna thwsncayaa yathccnatg | 420 |
| mgnyntnttya tgcartggca ygtwnsngtn athaargtnw sngtnatgta yytngaygay | 480 |
| gtnacncarw snrcarwsnyt naargargtn athacngayt tyytnacnca racncayaar | 540 |
| ytnwsnytnnt ayytntgyca racnatgaar gtnggnacna arggncngg ngayaayytn | 600 |
| caycargtng cncngayyt nytnytnccn garcaratha thaartayyt ntgyaarwsn | 660 |
| gargarttya tggayccngc nacttyath aayatgtaya aymgncnat hcayathacn | 720 |
| ytngaywsng argtngtntg gccngcncn wsnmgntty | 759 |

<210> 6
 <211> 759
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of mouse
z1mda24 shown in SEQ ID NO:4

<221> misc_feature

<222> (1)...(759)

<223> n = A,T,C or G

<400> 6

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|--|-----|
| atgwsnttya tggtnccayaa ymgnaarggn wsnaaraarc arttycargt ngayccnytn | 60 |
| ytnytnccna argtnccnmg nacnaaytay ytnccayytn argargaraa rcaymgnytn | 120 |
| carytnaara arttyytnyt ncaymgntg tyytngtn gntayathca rggnaayacn | 180 |
| garaaraarg ayathwsnga rtaytaygar carytnntyc arwsnathyt naarcaycay | 240 |
| ytngnggarw sngtnacngg nytnatgytn gntayccnw snacnttyt ncayathytn | 300 |
| garwsnwsna ayggnacnyt nttymgnath ytnytnngayt aygtngcnca ygaraarwsn | 360 |
| garacngart tyatgytnca raayatgaar athgtngtn cwnsnccayaa yathccnccn | 420 |
| mgnynttya tgcartggca yathwsngcn athaargtn cngtnytna yytnngaygay | 480 |
| garwsncarw snccnwsnat hgargargtn acnacngart tyytnacnat gacncayaar | 540 |
| ytngcnytn arytnayaa racngtnaar ytngngcna arggnccngg ngayaayytn | 600 |
| caycarytn cncngaryt nathytnccn garcaratha thaartayt ntgyaargcn | 660 |
| gargarttya tggayccngc nwsnttytn wsnatgtaya aymgnccnat hcaygtnacn | 720 |
| ytngaywsng ayathgtntg gccngcncn wsnmgntty | 759 |

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC29714

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| aacagaccca tacacgttac cctgg | 25 |
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<210> 8

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC29984

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| tcttgcccc ttctggctc ctg | 23 |
|-------------------------|----|

<210> 9
 <211> 23
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC21195

<400> 9
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<210> 10
 <211> 23
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<210> 11
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<400> 12

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<211> 24

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<223> Oligonucleotide primer ZC29567

<400> 16
cctcccagaa caaatcat 18

<210> 17
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<212> DNA
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<223> Oligonucleotide primer ZC29568

<400> 17
accacctcag aatccaga 18

<210> 18
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<223> Glu-Glu (CEE) Tag amino acid sequence

<400> 18
Glu Tyr Met Pro Met Glu
1 5

<210> 19
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<212> DNA
<213> Artificial Sequence

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<223> Oligonucleotide Sequence ZC29056

<400> 20

tgctctagag cgaaacgtga aggagcaggc cata

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<220>

<223> Oligonucleotide Sequence ZC447

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taacaatttc acacagg

17

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide Sequence ZC976

<400> 22

cgttgtaaaa cgacggcc

18

<210> 23

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Representative zlmda24 polypeptide containing
C-terminal Glu-Glu (CEE) tag

<400> 23

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| Met | Ser | Phe | Ser | Val | His | Asn | Gln | Lys | Gly | Ser | Lys | Arg | Pro | Leu | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Glu | Pro | Leu | Leu | Phe | Leu | Gln | Val | Pro | Arg | Ser | Asn | Tyr | Leu | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Gln | Glu | Glu | Lys | Gln | Arg | Leu | His | Leu | Lys | Lys | Phe | Leu | Leu | Asp |
| | | | 35 | | | | 40 | | | | | | 45 | | |

Arg Met Phe Leu Val Ala Lys Ile Gln Ala Asn Val Glu Arg Lys Asp
 50 55 60
 Val Ala Asp Tyr Tyr Glu Gln Met Phe Gln Ser Val Leu Lys His His
 65 70 75 80
 Leu Gly Glu Ala Val Thr Gly Leu Leu Leu Ile Tyr Pro Thr Ser Ile
 85 90 95
 Leu His Ile Leu Glu Ser Ser Ser Asp Thr Leu Tyr Lys Val Leu Leu
 100 105 110
 Asp Tyr Ile Gly His Val Lys Asp Glu Thr Val Phe Phe Ile Gln Gln
 115 120 125
 Met Lys Ile Ile Val Ile Ser His Asn Ile Pro Met Arg Leu Phe Met
 130 135 140
 Gln Trp His Val Ser Val Ile Lys Val Pro Val Met Tyr Leu Asp Asp
 145 150 155 160
 Val Thr Gln Ser Gln Ser Leu Lys Glu Val Ile Thr Asp Phe Leu Thr
 165 170 175
 Gln Thr His Lys Leu Ser Leu Tyr Leu Cys Gln Thr Met Lys Val Gly
 180 185 190
 Thr Lys Gly Pro Gly Asp Asn Leu His Gln Val Ala Pro Asp Leu Leu
 195 200 205
 Leu Pro Glu Gln Ile Ile Lys Tyr Leu Cys Lys Ser Glu Glu Phe Met
 210 215 220
 Asp Pro Ala Thr Phe Ile Asn Met Tyr Asn Arg Pro Ile His Ile Thr
 225 230 235 240
 Leu Asp Ser Glu Val Val Trp Pro Ala Pro Ser Arg Phe Ala Leu Glu
 245 250 255
 Tyr Met Pro Met Glu
 260

<210> 24

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Sequence ZC29127

<400> 24

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32

<210> 25

<211> 32

<212> DNA

$\langle 220 \rangle$

<400> 25

32